

1 ATGCTGTTCCGCGCCCGGGGGCCGGTACGGGGCAGGGGCTGGGGCGGCGGCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20

 61 CCCC GCCGCGGGGCGCTCGCCGCCCTGGAGCCCCGCTGGATTGCTGCTGGGCGCTCGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40

 121 GGCTGCCAGGCGGGCGCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCCGCCGCTTCCTCCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60

 181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG 240
 61 C Q E K D Y H F E Y T E C D S S G S R W 80

 241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300
 81 R V A I P N S A V D C S G L P D P V R G 100

 301 AAAGAATGCACTTTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120

 361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140

 421 GAATTGCCGCGCAGGATTTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCCCTTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160

 481 GACAGCAGGCCAGACGGCTGTAACAACTCTTCTTGATCCCTCGTGGAACCTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180

 541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200

 601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

FIG. 1A

661 AATGATCAGTGCCAGGAGATGGACACCACCACTGACAAGTGGGTAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240
 721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260
 781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280
 841 ATTGAAGCGGTGGCGTACACATCAGAATGTTTTCTTGCAAGCCAGGCACATTCAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300
 901 AAACCAGGTTTCACTCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320
 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340
 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360
 1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAATCTGCCGGGAGCATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380
 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATTT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400
 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCCTCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440

FIG. 1B

1321 TGG AATGTCCTTCCTGGCAACATGAAAACCTCCTGCTTCAATGTTGCGAATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460

1381 GATGGAATGAATGGTTGGGACGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

1441 GACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTCGGGTTTCATCGTGTGTCCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGCAACGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGCGGGCCTGGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

FIG. 1C

1981 AACAAATCAGGACCATTTCGGTTTGCTATAGTGAAGTCTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680

2041 CAGATTTTGCACATATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700

2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

2161 GAGCGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
 721 E G K K M A L C T N N I T D F T V K E I 740

2221 GTGGCAGGGTCAGATGATTACACAAATTTGGTAGGGGCATTTGTATGCCAGTCAACAATT 2280
 741 V A G S D D Y T N L V G A F V C Q S T I 760

2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
 761 I P S E S K G F R A A L S S Q S I I L A 780

2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAGAAGAT 2400
 781 D T F I G V T V E T T L K N I N I K E D 800

2401 ATGTTCCCAGTTCCAACAAGCCAAATACCAGATGTGCATTTCTTTTATAAGTCTTCTACA 2460
 801 M F P V P T S Q I P D V H F F Y K S S T 820

2461 GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
 821 A T T S C I N G R S T A V K M R C N P T 840

2521 AAATCTGGAGCAGGAGTGATTTTCAGTCCCCAGCAAGTGGCCAGCAGGTACCTGTGATGGG 2580
 841 K S G A G V I S V P S K C P A G T C D G 860

2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC 2640
 861 C T F Y F L W E S A E A C P L C T E H D 880

FIG. 1D

2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTTGAGGAAACCTTGTATGTGTGGAAT 2700
 881 F H E I E G A C K R G F Q E T L Y V W N 900
 2701 GAACCTAAATGGTGCATTAAAGGAATTTCTTTGCCTGAGAAAAAGTTGGCAACCTGTGAA 2760
 901 E P K W C I K G I S L P E K K L A T C E 920
 2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTGTCTG 2820
 921 T V D F W L K V G A G V G A F T A V L L 940
 2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAGAAAAAGAAGACCATTTTGAAT 2880
 941 V A L T C Y F W K K N Q K K K K T I L N 960
 2881 CTGTTCAACTGAAAACCTCAAGATCCCCAAATATATGAAGAGACAGTGCTGTAGCCTTGA 2940
 961 L F N * 964
 2941 GACTAATGAACAAAGAAACCTGCTCTAGTTTTACAGGACCATATTTTAGGGTCTGTCCTC 3000
 3001 ATACCTGTCACATTGCTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGGAAGGAGAT 3060
 3061 TGAAACATTTGATTGCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAAT 3120
 3121 GATTTGGGTCTCAACTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACAC 3180
 3181 ATAAGTGAAGAACCAAGTTTAAAGCCCAATGCACTGCTGATGCATGCCATATAATTAAT 3240
 3241 GGGTAACTTTTATCTTTATGATGTCTACATAACAAGTGTGATTTGGAAGGCACATGTGA 3300
 3301 GCATATGCATTATGATCCAATTTATGTTTTTCTTTGTTTATATTTTGGGAAAATTAAA 3360
 3361 ATTTTTTTAAGGTAAAAA 3390

FIG. 1E

FIG. 2A

| | | | | | | | | | | | | | | |
|-----|---|---|-----|-----|---|---|---|---|---|---|---|---------|------------|------|
| | | 10 | 20 | 30 | | | | | | | | | | |
| 1 | | M L F R A R G P V R G R G W G R P A E A P R R G R S P F W S | | | | | | | | | | TR16.aa | | |
| 1 | M | - | - | - | - | - | - | - | - | - | D I K N L - L T V - - - | EMB | CAB41042.1 | TNFR |
| 1 | M | - | - | - | - | - | - | - | - | - | C V G A R R L G R G P - - - | emb | CAA53576.1 | OX40 |
| | | 40 | 50 | 60 | | | | | | | | | | |
| 31 | | P A W I C C W A L A G C Q A A W A G D L P S S S S R B L P P | | | | | | | | | | TR16.aa | | |
| 10 | - | - | - | - | - | - | - | - | - | - | C T I F Y I T T L A T A D - - - - - | EMB | CAB41042.1 | TNFR |
| 13 | - | - | - | - | - | - | - | - | - | - | C A A L L L L G L G L S T - - - - - | emb | CAA53576.1 | OX40 |
| | | 70 | 80 | 90 | | | | | | | | | | |
| 61 | | C O E K D Y H F E Y T E C D S S G S R W R V A I P N S A V D | | | | | | | | | | TR16.aa | | |
| 23 | - | - | - | - | - | - | - | - | - | - | I P T S S L P - - - - - | EMB | CAB41042.1 | TNFR |
| 26 | - | - | - | - | - | - | - | - | - | - | V - - T G L H - - - - - | emb | CAA53576.1 | OX40 |
| | | 100 | 110 | 120 | | | | | | | | | | |
| 91 | | C S G L P D P V R G K E C T F S C A S G E Y L E M K N O V C | | | | | | | | | | TR16.aa | | |
| 30 | - | - | - | - | - | - | - | - | - | - | H A P V N G - - - - - A C D E G E Y L D K R H N Q C | EMB | CAB41042.1 | TNFR |
| 31 | - | - | - | - | - | - | - | - | - | - | C V G D T Y - - P S N D R C - - - - - | emb | CAA53576.1 | OX40 |
| | | 130 | 140 | 150 | | | | | | | | | | |
| 121 | | S K C G E G T Y S L G S G I K F D E W D E L P A G F S N I A | | | | | | | | | | TR16.aa | | |
| 51 | - | - | - | - | - | - | - | - | - | - | - - - - - | EMB | CAB41042.1 | TNFR |
| 43 | - | - | - | - | - | - | - | - | - | - | - - - - - | emb | CAA53576.1 | OX40 |
| | | 160 | 170 | 180 | | | | | | | | | | |
| 151 | | T F M D T V V G P S D S R P D G C N N S S W I P R G N Y I E | | | | | | | | | | TR16.aa | | |
| 51 | - | - | - | - | - | - | - | - | - | - | - - - - - | EMB | CAB41042.1 | TNFR |
| 43 | - | - | - | - | - | - | - | - | - | - | - - - - - | emb | CAA53576.1 | OX40 |
| | | 190 | 200 | 210 | | | | | | | | | | |
| 181 | | S N R D D C T V S L I Y A V H L K K S G Y V F F E Y O Y V D | | | | | | | | | | TR16.aa | | |
| 51 | - | - | - | - | - | - | - | - | - | - | - - - - - | EMB | CAB41042.1 | TNFR |
| 43 | - | - | - | - | - | - | - | - | - | - | - - - - - | emb | CAA53576.1 | OX40 |
| | | 220 | 230 | 240 | | | | | | | | | | |
| 211 | | N N I F F E F F I O N D O C O E M D T T T D K W V K L T D N | | | | | | | | | | TR16.aa | | |
| 51 | - | - | - | - | - | - | - | - | - | - | - - - - - | EMB | CAB41042.1 | TNFR |
| 43 | - | - | - | - | - | - | - | - | - | - | - - - - - | emb | CAA53576.1 | OX40 |
| | | 250 | 260 | 270 | | | | | | | | | | |
| 241 | | G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A | | | | | | | | | | TR16.aa | | |
| 51 | - | - | - | - | - | - | - | - | - | - | - - - - - | EMB | CAB41042.1 | TNFR |
| 43 | - | - | - | - | - | - | - | - | - | - | - - - - - | emb | CAA53576.1 | OX40 |
| | | 280 | 290 | 300 | | | | | | | | | | |
| 271 | | V K P V L V K N I T I E G V A Y T S E C F P C K P G T F S N | | | | | | | | | | TR16.aa | | |
| 51 | - | - | - | - | - | - | - | - | - | - | C N Q C P P G E F A K - - - - - | EMB | CAB41042.1 | TNFR |
| 43 | - | - | - | - | - | - | - | - | - | - | C H E C R P G N G M V - - - - - | emb | CAA53576.1 | OX40 |
| | | 310 | 320 | 330 | | | | | | | | | | |
| 301 | | K P G S F N C O V C P R N T Y S E K G A K E C I R C K D D S | | | | | | | | | | TR16.aa | | |
| 62 | - | - | - | - | - | - | - | - | - | - | V R C N - - - - - | EMB | CAB41042.1 | TNFR |
| 54 | - | - | - | - | - | - | - | - | - | - | S R C S - - - - - | emb | CAA53576.1 | OX40 |

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FIG. 2B

| | 340 | 350 | 360 | |
|-----|---|-----|-----|---------------------|
| 331 | Q F S G S S E C T E R P P C T T K D Y F Q I H T P C D E E G | | | TR16.aa |
| 66 | - | | | EMB CAB41042.1 TNFR |
| 58 | - | | | emb CAA53576.1 OX40 |
| | 370 | 380 | 390 | |
| 361 | K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K | | | TR16.aa |
| 66 | - | | | EMB CAB41042.1 TNFR |
| 58 | - | | | emb CAA53576.1 OX40 |
| | 400 | 410 | 420 | |
| 391 | K D C P P C N P G F Y N N G S S S C H P C P P G T F S D G T | | | TR16.aa |
| 70 | T K C E R C P P H T Y T A I P N Y S N G C - - - - - | | | EMB CAB41042.1 TNFR |
| 62 | T V C R P C G P G F Y N D V V S - S K P C - - - - - | | | emb CAA53576.1 OX40 |
| | 430 | 440 | 450 | |
| 421 | K E C R P C P A G T E P A L G F E Y K W W N V L P G N M K T | | | TR16.aa |
| 91 | H Q C R K C - - P T G S - - - - - F D K V | | | EMB CAB41042.1 TNFR |
| 82 | K P C T W C N L R S G S - - - - - E R K Q | | | emb CAA53576.1 OX40 |
| | 460 | 470 | 480 | |
| 451 | S C F N V G N S K C D G M N G W E V A G D H I Q S G A G G S | | | TR16.aa |
| 105 | K C T G T Q N S K C S C L P G W Y C A T D S S Q T - - - - - | | | EMB CAB41042.1 TNFR |
| 98 | L C T A T Q D T V C R C R A G - - - - - T Q P L D S - - - - - | | | emb CAA53576.1 OX40 |
| | 490 | 500 | 510 | |
| 481 | D N D Y L I L N L H I P G F K E P T S M T G A T G S E L G R | | | TR16.aa |
| 130 | - | | | EMB CAB41042.1 TNFR |
| 119 | - | | | emb CAA53576.1 OX40 |
| | 520 | 530 | 540 | |
| 511 | I T F V F E T L C S A D C V L Y F M V D I N R K S T N V V E | | | TR16.aa |
| 132 | - | | | EMB CAB41042.1 TNFR |
| 122 | - | | | emb CAA53576.1 OX40 |
| | 550 | 560 | 570 | |
| 541 | S W G G T K E K Q A Y T H I I F K N A T F T F T W A F O R T | | | TR16.aa |
| 137 | - | | | EMB CAB41042.1 TNFR |
| 127 | - | | | emb CAA53576.1 OX40 |
| | 580 | 590 | 600 | |
| 571 | N O G O D N R R F I N D M V K I Y S I T A T N A V D G V A S | | | TR16.aa |
| 137 | - | | | EMB CAB41042.1 TNFR |
| 127 | - | | | emb CAA53576.1 OX40 |
| | 610 | 620 | 630 | |
| 601 | S C R A C A L G S E Q S G S S Q V P C P P G H Y I E K E T N | | | TR16.aa |
| 141 | - | | | EMB CAB41042.1 TNFR |
| 128 | - | | | emb CAA53576.1 OX40 |

FIG. 2C

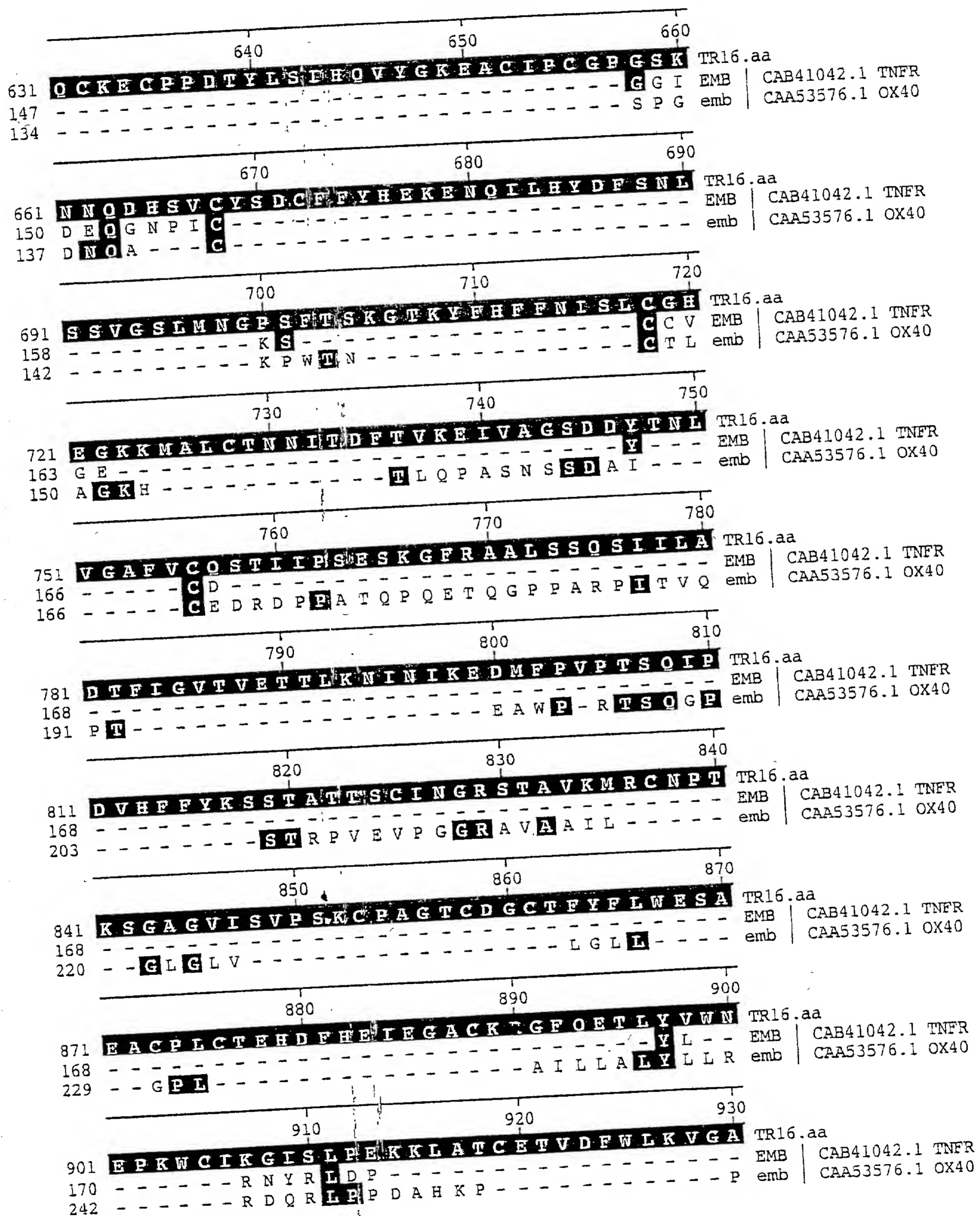


FIG. 2D

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|---|-----|---|-----|---|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---------|---|-----|------------|------|
| | | 940 | | 950 | | 960 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 931 | G | V | G | A | E | T | A | V | L | L | V | A | L | T | C | Y | F | W | K | N | Q | K | K | K | T | I | L | N | TR16.aa | | | | |
| 177 | - | - | - | - | F | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | P | P | C | K | L | S | EMB | CAB41042.1 | TNFR |
| 255 | G | G | G | S | F | R | T | P | I | - | - | - | - | - | - | - | - | - | Q | E | E | Q | A | D | A | H | S | T | L | A | emb | CAA53576.1 | OX40 |

961 L F N
 184 K C - N
 276 K I

TR16.aa
 EMB CAB41042.1 TNFR
 emb CAA53576.1 OX40

TR16.aa

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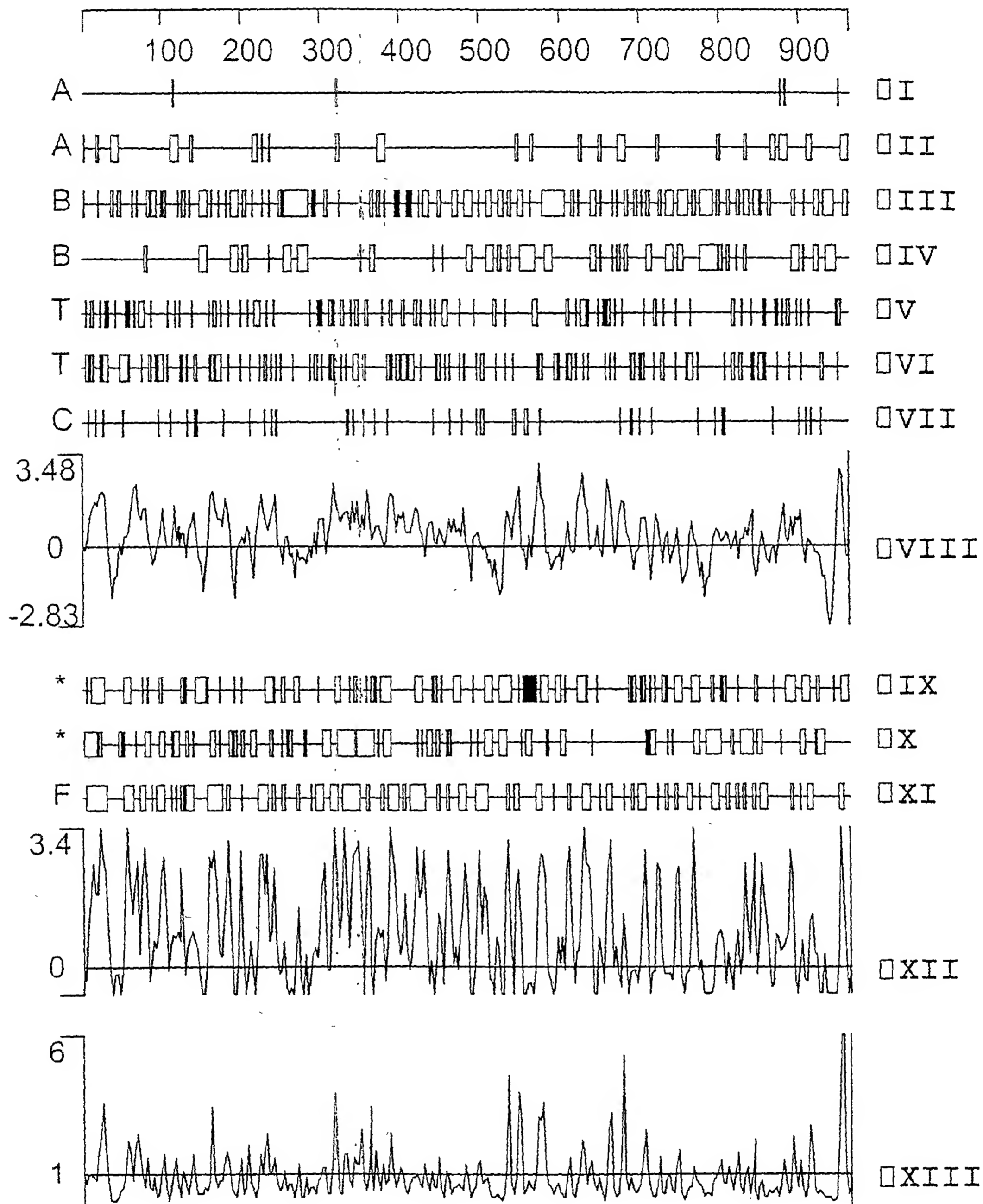


FIG. 3

1 ATGCTGTTCCGCGCCCGGGGGCCGGTACGGGGCAGGGCTCGGGGCGCGCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20
 61 CCGCGCGCGGGCGCTCGCGCCCTGGAGCCCCGCTGGATTGCTGCTGGGCGCTCGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40
 121 GGCTGCCAGGCGGCCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCGCGCGCTTCCTCCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60
 181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG 240
 61 C Q E K D Y H F E Y T E C D S S G S R W 80
 241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300
 81 R V A I P N S A W D C S G L P D P V R G 100
 301 AAAGAATGCACTTTCTCCTGTCTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120
 361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140
 421 GAATTGCCGGCAGGATTTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCCCCTTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160
 481 GACAGCAGGCCAGACGGCTGTAACAACTCTTCTTGGATCCCTCGTGGAACCTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180
 541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200
 601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220
 661 AATGATCAGTGCCAGGAGATGACACCACCACTGACAAGTGGGTAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240

FIG. 4A

721 GGACAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260
 781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280
 841 ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCCTTGCAAGCCAGGCACATTCAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300
 901 AAACCAGGTTCACTCAACTGCCAGGTGTGTCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320
 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGACTGTACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340
 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360
 1081 AAGACACAGATAATGTACAAGTGCATAGAGCCCAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380
 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATTT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400
 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440
 1321 TGGAATGTCCTTCTGGAACATGAAAACCTTCTGCTTCAATGTTGGGAATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460
 1381 GATGGAATGAATGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

FIG. 4B

1441 GACAATGATTACCTGATCTTAACTTGCATATCCCAGGATTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500
 1501 ACTGGAGCCACGGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520
 1561 GCTGACTGTGTTTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540
 1621 TCGTGGGGTGGAAACCAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560
 1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580
 1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600
 1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTCGGGTTTCATCGTGTGTCCTGCCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620
 1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGCAAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640
 1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGCGGGCCTGGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660
 1981 AACAAATCAGGACCATTGCGTTTGCTATAGTGACTGCTTTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V E Y S D C F F Y H E K E N 680
 2041 CAGATTTTGCCTATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700
 2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

FIG. 4C

2161 GAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
 721 E G K K M A L C T N N I T D F T V K E I 740
 2221 GTGGCAGGGTCAGATGATTACACAAATTTGGTAGGGGCATTTGTATGCCAGTCAACAATT 2280
 741 V A G S D D Y T N L V G A F V C Q S T I 760
 2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
 761 I P S E S K G F R A A L S S Q S I I L A 780
 2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAAGAAGAT 2400
 781 D T F I G V T V E T T L K N I N I K E D 800
 2401 ATGTTCCCAGTTCCAACAAGCAAATACCAGATGTGCATTTCTTTTATAAGTCTTCTACA 2460
 801 M F P V P T S Q I P D V H F F Y K S S T 820
 2461 GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
 821 A T T S C I N G R S T A V K M R C N P T 840
 2521 AAATCTGGAGCAGGAGTGATTTCACTCCCCAGCAAGTGCCCAGCAGGTACCTGTGATGGG 2580
 841 K S G A G V I S V P S K C P A G T C D G 860
 2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC 2640
 861 C T F Y F L W E S A E A C P L C T E H D 880
 2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTTCAAGAAACCTTGTATGTGTGGAAT 2700
 881 F H E I E G A C K R G F Q E T L Y V W N 900
 2701 GAACCTAAATGGTGCATTAAAGGAATTTCTTTGCCTGAGAAAAAGTTGGCAACCTGTGAA 2760
 901 E P K W C I K G I S L P E K K L A T C E 920
 2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGCAGCTTTTACTGCCGTTTGTCTG 2820
 921 T V D F W L K V G A G V G A F T A V L L 940
 2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAAGTGAATACAAATATTCCAAG 2880
 941 V A L T C Y F W K K N Q K L E Y K Y S K 960

FIG. 4D

2881 TTAGTAATGACGACTAACTCAAAAGAGTGTGAACTCCCGGCTGCAGACAGTTGTGCTATC 2940
961 L V M T T N S K E C E L P A A D S C A I 980

2941 ATGGAAGGAGAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACAGTCACTACTAGGA 3000
981 M E G E D N E E E V V Y S N K Q S L L G 1000

3001 AAACTCAAATCTTTGGCAACCAAGGAAAAAGAAGACCATTTTGAATCTGTTCAACTGAAA 3060
1001 K L K S L A T K E K E D H F E S V Q L K 1020

3061 ACCTCAAGATCCCCAAATATATGAAGAGACAGTGTGTAGCCTTGAGACTAATGAACAAA 3120
1021 T S R S P N I * 1028

3121 GAAACCTGCTCTAGTTTTACAGGACCATATTTTAGGGTCTGTCCTCATACCTGTCACATT 3180

3181 GGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGGAAGGAGATTGAAACATTTGATT 3240

3241 GCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAATGATTTGGCTCTCAA 3300

3301 CTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACACATAACTGAAAACCA 3360

3361 AGTTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAATGGGTAACTTTTATT 3420

3421 CTTTATGATGTCTACATAACAAGTGTGATTTGGAAGGCACATCTGAGCATATGCATTATG 3480

3481 ATCCAATTTATGTTTTTTCTTTGTTTATATTTTGGGAAAATTAAAAATTTTTTAAGGTA 3540

3541 AAAAAAAAAAAAAAAAAA 3556

FIG. 4E

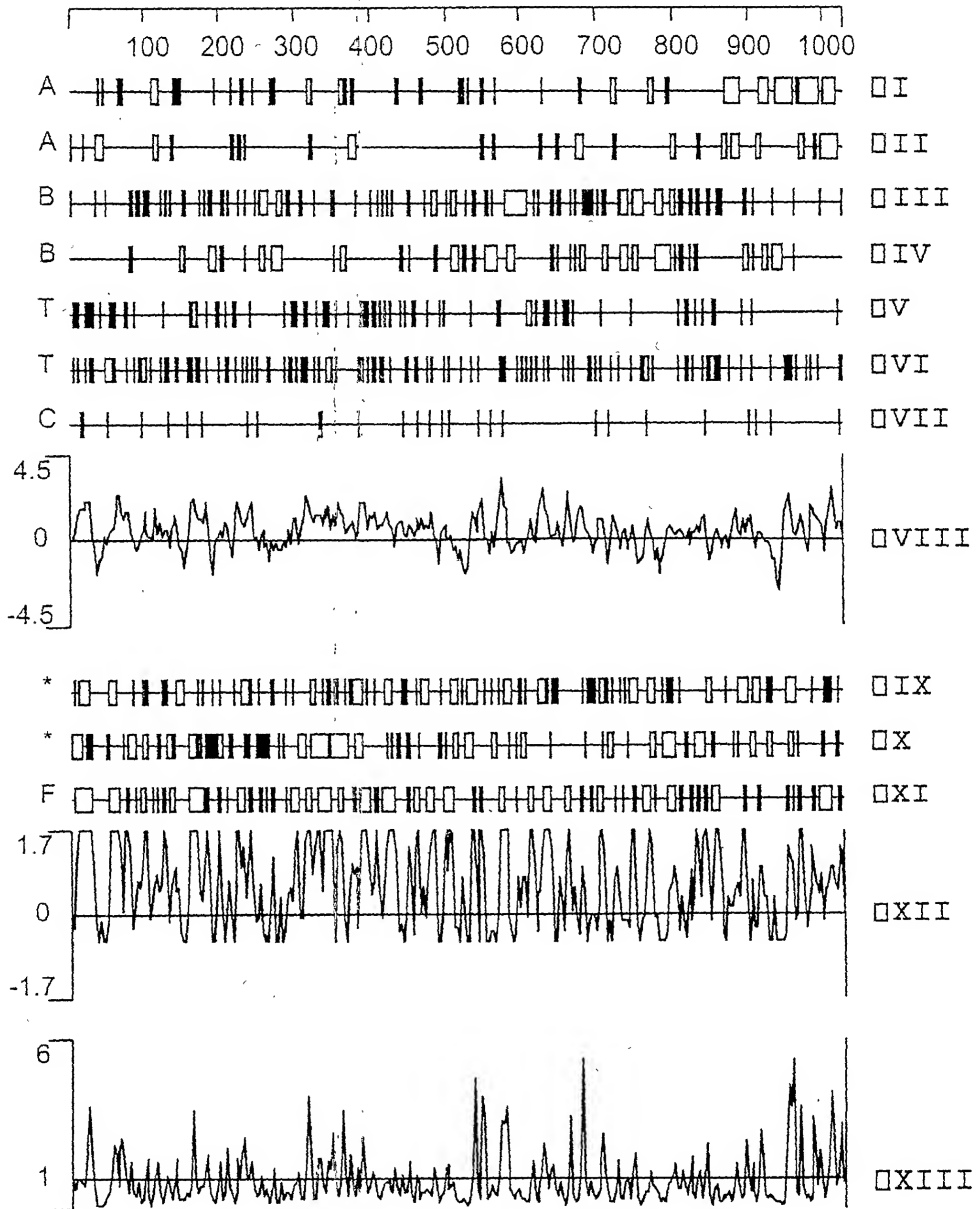


FIG. 5

| | | | | | |
|-----|---|-----|-----|-----|----------|
| | 10 | 20 | 30 | 40 | |
| 1 | MLFRARGPVRGRGWGRPAEAPRRGRSPPWSPA WICCWALA | | | | SEQ ID 2 |
| 1 | ----- | | | | SEC10 |
| | 50 | 60 | 70 | 80 | |
| 41 | GCQAAWAGDLPSSSSRPLPPCQEKDYHFEYTECDSSGSRW | | | | SEQ ID 2 |
| 1 | ----- | | | | SEC10 |
| | 90 | 100 | 110 | 120 | |
| 81 | RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLEMKNQVC | | | | SEQ ID 2 |
| 1 | -----MKNQVC | | | | SEC10 |
| | 130 | 140 | 150 | 160 | |
| 121 | SKCGEGTYSLSGSGIKFDEWDELPAGFSNIATFMDTVVGPS | | | | SEQ ID 2 |
| 7 | SKCGEGTYSLSGSGIKFDEWDELPAGFSNIATFMDTVVGPS | | | | SEC10 |
| | 170 | 180 | 190 | 200 | |
| 161 | DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKSG | | | | SEQ ID 2 |
| 47 | DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKSG | | | | SEC10 |
| | 210 | 220 | 230 | 240 | |
| 201 | YVFFEYQYVDNNIFFEFFIQNDQCQEMDTTTDKWVKLTDN | | | | SEQ ID 2 |
| 87 | YVFFEYQYVDNNIFFEFFIQNDQCQEMDTTTDKWVKLTDN | | | | SEC10 |
| | 250 | 260 | 270 | 280 | |
| 241 | GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT | | | | SEQ ID 2 |
| 127 | GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT | | | | SEC10 |
| | 290 | 300 | 310 | 320 | |
| 281 | IEGVAYTSECFPCPKPGTFSNKP GSFNCQVCP RNTYSEKGA | | | | SEQ ID 2 |
| 167 | IEGVAYTSECFPCPKPGTFSNKP GSFNCQVCP RNTYSEKGA | | | | SEC10 |
| | 330 | 340 | 350 | 360 | |
| 321 | KECIRCKDDSOFS--GSSECTERPPCTTKDYFOIHTPCDE | | | | SEQ ID 2 |
| 207 | KECIRCKDDSOFS EE GSSECTERPPCTTKDYFOIHTPCDE | | | | SEC10 |
| | 370 | 380 | 390 | 400 | |
| 359 | EGKTQIMYKWIEPKICREDLTDAIRLPSPGEEKKDCPPCNP | | | | SEQ ID 2 |
| 247 | EGKTQIMYKWIEPKICREDLTDAIRLPSPGEEKKDCPPCNP | | | | SEC10 |
| | 410 | 420 | 430 | 440 | |
| 399 | GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGF EY | | | | SEQ ID 2 |
| 287 | GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGF EY | | | | SEC10 |
| | 450 | 460 | 470 | 480 | |
| 439 | KWWNVLPGNMKTSCFN VGNSKCDGMNGWEVAGDHIQSGAG | | | | SEQ ID 2 |
| 327 | KWWNVLPGNMKTSCFN VGNSKCDGMNGWEVAGDHIQSGAG | | | | SEC10 |
| | 490 | 500 | 510 | 520 | |
| 479 | GSDNDYLILNLHIPGFKPPTSMTGATGSELGRITFVFETL | | | | SEQ ID 2 |
| 367 | GSDNDYLILNLHIPGFKPPTSMTGATGSELGRITFVFETL | | | | SEC10 |

FIG. 6A

| | | |
|-----|--|----------|
| 519 | CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN | SEQ ID 2 |
| 407 | CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN | SEC10 |
| 559 | ATFTFTWAFQRTNQGGQDNRRFINDMVKIYSITATNAVDGV | SEQ ID 2 |
| 447 | ATFTFTWGIPRE----- | SEC10 |
| 599 | ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD | SEQ ID 2 |
| 459 | ----- | SEC10 |
| 639 | TYLSIHQVYGKEACIPCGPGSKNNQDHSVCSDCFFYHEK | SEQ ID 2 |
| 459 | ----- | SEC10 |
| 679 | ENQILHYDFSNLSSVGS LMNGPS SFTSKGTYFHHFFNISLC | SEQ ID 2 |
| 459 | ----- LIQGR | SEC10 |
| 719 | GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFCQS | SEQ ID 2 |
| 464 | | SEC10 |
| 759 | TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK | SEQ ID 2 |
| 464 | | SEC10 |
| 799 | EDMFPVPTSQIPDVHFFYKSSTATTSCTINGRSTAVKMRCN | SEQ ID 2 |
| 464 | | SEC10 |
| 839 | PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE | SEQ ID 2 |
| 464 | | SEC10 |
| 879 | HDFHEIEGACKRGFQETLYVWNEPKWCIGISLPEKKLAT | SEQ ID 2 |
| 464 | | SEC10 |
| 919 | CETVDFWLKVGAGVGAF TAVLLVALTCYFWKKNQKKKKT I | SEQ ID 2 |
| 464 | | SEC10 |
| 959 | LNLFN | SEQ ID 2 |
| 464 | | SEC10 |

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B

| | | | | | | |
|-----|--|--|-----|-----|-----|----------|
| | | 10 | 20 | 30 | 40 | |
| 1 | | MLFRARGPVRGRGWGRPAPRRGRSPPWSPA WICCWALA | | | | SEQ ID 4 |
| 1 | | ----- | | | | SEC10 |
| | | 50 | 60 | 70 | 80 | |
| 41 | | GCQA AWAGDLPSSSSRPLPPCQEKDYHFEYTECDSSGSRW | | | | SEQ ID 4 |
| 1 | | ----- | | | | SEC10 |
| | | 90 | 100 | 110 | 120 | |
| 81 | | RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLEMKNQVC | | | | SEQ ID 4 |
| 1 | | -----MKNQVC | | | | SEC10 |
| | | 130 | 140 | 150 | 160 | |
| 121 | | SKCGEGTYSLSGSGIKFDEWDELPA GFSNIATFMDTVVGPS | | | | SEQ ID 4 |
| 7 | | SKCGEGTYSLSGSGIKFDEWDELPA GFSNIATFMDTVVGPS | | | | SEC10 |
| | | 170 | 180 | 190 | 200 | |
| 161 | | DSRPDGCNNSSWIPRGN YIESNRDDCTVSLIYAVHLKKSG | | | | SEQ ID 4 |
| 47 | | DSRPDGCNNSSWIPRGN YIESNRDDCTVSLIYAVHLKKSG | | | | SEC10 |
| | | 210 | 220 | 230 | 240 | |
| 201 | | YVFFEYQYVDNNIFFEFFIQNDQCQEMD TTTDKWVKLTDN | | | | SEQ ID 4 |
| 87 | | YVFFEYQYVDNNIFFEFFIQNDQCQEMD TTTDKWVKLTDN | | | | SEC10 |
| | | 250 | 260 | 270 | 280 | |
| 241 | | GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPV LVKNIT | | | | SEQ ID 4 |
| 127 | | GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPV LVKNIT | | | | SEC10 |
| | | 290 | 300 | 310 | 320 | |
| 281 | | IEGVAYTSECFPCPKPGTFSNKP GSFNCQVCPRNTYSEKGA | | | | SEQ ID 4 |
| 167 | | IEGVAYTSECFPCPKPGTFSNKP GSFNCQVCPRNTYSEKGA | | | | SEC10 |
| | | 330 | 340 | 350 | 360 | |
| 321 | | KECIRCKDDSQFS --GSSECTERPPCTTKDYFOIHTPCDE | | | | SEQ ID 4 |
| 207 | | KECIRCKDDSQFS EE GSSECTERPPCTTKDYFOIHTPCDE | | | | SEC10 |
| | | 370 | 380 | 390 | 400 | |
| 359 | | EGKTOIMYKWIEPKICREDLTDAIRLP PSGEKKDCPPCNP | | | | SEQ ID 4 |
| 247 | | EGKTOIMYKWIEPKICREDLTDAIRLP PSGEKKDCPPCNP | | | | SEC10 |
| | | 410 | 420 | 430 | 440 | |
| 399 | | GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGFEY | | | | SEQ ID 4 |
| 287 | | GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGFEY | | | | SEC10 |
| | | 450 | 460 | 470 | 480 | |
| 439 | | KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG | | | | SEQ ID 4 |
| 327 | | KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG | | | | SEC10 |
| | | 490 | 500 | 510 | 520 | |
| 479 | | GSDNDYLILNLHIPGFKPPTSMTGATGSELGRITFVFETL | | | | SEQ ID 4 |
| 367 | | GSDNDYLILNLHIPGFKPPTSMTGATGSELGRITFVFETL | | | | SEC10 |

FIG. 7A

| | | |
|-----|--|----------|
| 519 | CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHLIFKN | SEQ ID 4 |
| 407 | CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHLIFKN | SEC10 |
| 559 | ATFTFTWAFQR | SEQ ID 4 |
| 447 | ATFTFTWGI PRE | SEC10 |
| 599 | ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD | SEQ ID 4 |
| 459 | ----- | SEC10 |
| 639 | TYLSIHQVYGKEACIPCGPGSKNNQDHSVCSDCFFYHEK | SEQ ID 4 |
| 459 | ----- | SEC10 |
| 679 | ENQILHYDFS NLSSVGS LMNGPS | SEQ ID 4 |
| 459 | ----- LIQGP | SEC10 |
| 719 | GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS | SEQ ID 4 |
| 464 | ----- | SEC10 |
| 759 | TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK | SEQ ID 4 |
| 464 | ----- | SEC10 |
| 799 | EDMFPVPTSQIPDVHFFYKSSTATTSCTINGRSTAVKMR CN | SEQ ID 4 |
| 464 | ----- | SEC10 |
| 839 | PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE | SEQ ID 4 |
| 464 | ----- | SEC10 |
| 879 | HDFHEIEGACKRGRFQETLYVWNEPKWCIGISLPEKKLAT | SEQ ID 4 |
| 464 | ----- | SEC10 |
| 919 | CETVDFWLKV GAGVGAF TAVLLVALTCYFWKKNQKLEYKY | SEQ ID 4 |
| 464 | ----- | SEC10 |
| 959 | SKLVMTTNSKECELPAAADSCAIMEGEDNEEEVVYSNKQSL | SEQ ID 4 |
| 464 | ----- | SEC10 |
| 999 | LGKLSLATKEKEDHFE SVQLKTSRSPNI | SEQ ID 4 |
| 464 | ----- R | SEC10 |

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B